

#6/a

SEQUENCE LISTING

<110> Waldmann, Rainer

<120> MAMMAL NEURONAL ACID SENSING CATIONIC
CHANNEL, CLONING AND APPLICATIONS THEREOF

<130> 989.6701P

<140> 09/129,758

<141> 1998-08-05

<150> PCT/FR98/00270

<151> 1998-02-11

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<150> FR 97/09587

<151> 1997-07-28

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<170> PatentIn Ver. 2.0

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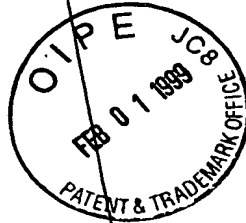
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Thr	Cys	Asp	Thr	Met	Pro	Asn	His	Ser	Glu	Thr	Ile	Ser	His	Thr	Val	485	490	495	
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 Asn Cys Asn Cys Arg Met Val His Met Pro Gly Asp Ala Pro Tyr Cys
 355 360 365
 Thr Pro Glu Gln Tyr Lys Glu Cys Ala Asp Pro Ala Leu Asp Phe Leu
 370 375 380
 Val Glu Lys Asp Gln Glu Tyr Cys Val Cys Glu Met Pro Cys Asn Leu
 385 390 395 400
 Thr Arg Tyr Gly Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys Ala
 405 410 415
 Ser Ala Lys Tyr Leu Ala Lys Lys Phe Asn Lys Ser Glu Gln Tyr Ile
 420 425 430
 Gly Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Val Leu Asn Tyr
 435 440 445

Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Ile Ala Gly Leu Leu Gly
 450 455 460
 Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Ile Leu Thr
 465 470 475 480
 Val Leu Glu Leu Phe Asp Tyr Ala Tyr Glu Val Ile Lys His Arg Leu
 485 490 495
 Cys Arg Arg Gly Lys Cys Gln Lys Glu Ala Lys Arg Ser Ser Ala Asp
 500 505 510
 Lys Gly Val Ala Leu Ser Leu Asp Asp Val Lys Arg His Asn Pro Cys
 515 520 525
 Glu Ser Leu Arg Gly His Pro Ala Gly Met Thr Tyr Ala Ala Asn Ile
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<213> rat

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<222> (1)..(1599)

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gac atc cgg gtg ttt gcc agc agc tgc aca atg cat ggt ctg ggc cac	96
Asp Ile Arg Val Phe Ala Ser Ser Cys Thr Met His Gly Leu Gly His	
20 25 30	
atc ttt ggc cct gga ggc ctg acc ctg cgc cga ggg ctg tgg gcc aca	144
Ile Phe Gly Pro Gly Gly Leu Thr Leu Arg Arg Gly Leu Trp Ala Thr	
35 40 45	
gct gtg ctc ctg tcg ctg gcg gcc ttc ctc tac cag gtg gct gag cgg	192
Ala Val Leu Leu Ser Leu Ala Ala Phe Leu Tyr Gln Val Ala Glu Arg	
50 55 60	
gtt cgc tac tat ggg gag ttc cac cat aag acc acc ctg gat gag cgt	240
Val Arg Tyr Tyr Gly Glu Phe His His Lys Thr Thr Leu Asp Glu Arg	
65 70 75 80	
gag agc cac cag ctc acc ttc cca gct gtg act ctg tgt aat atc aac	288
Glu Ser His Gln Leu Thr Phe Pro Ala Val Thr Leu Cys Asn Ile Asn	
85 90 95	
cca ctg cgc cgc tca cgc ctc aca ccc aat gac ttg cac tgg gct gga	336
Pro Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp Leu His Trp Ala Gly	
100 105 110	

aca gcg ctg ctg ggc ctg gac cct gct gaa cat gct gcc tac ctt cgt	384
Thr Ala Leu Leu Gly Leu Asp Pro Ala Glu His Ala Ala Tyr Leu Arg	
115 120 125	
gca ctg ggc cag ccc ccc gca cca cct ggc ttc atg ccc agt ccg acc	432
Ala Leu Gly Gln Pro Pro Ala Pro Pro Gly Phe Met Pro Ser Pro Thr	
130 135 140	
ttt gac atg gca caa ctc tac gcc aga gcc ggc cac tcc ctt gag gac	480
Phe Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly His Ser Leu Glu Asp	
145 150 155 160	
atg ttg ttg gat tgc cga tac cgt ggc cag ccc tgt ggg cct gag aac	528
Met Leu Leu Asp Cys Arg Tyr Arg Gly Gln Pro Cys Gly Pro Glu Asn	
165 170 175	
ttc aca gtg atc ttt act cga atg ggg caa tgc tac acc ttc aac tct	576
Phe Thr Val Ile Phe Thr Arg Met Gly Gln Cys Tyr Thr Phe Asn Ser	
180 185 190	
ggt gcc cac ggt gca gag ctg ctc acc act cca aag ggt ggt gct ggc	624
Gly Ala His Gly Ala Glu Leu Leu Thr Thr Pro Lys Gly Gly Ala Gly	
195 200 205	
aac gga ctg gag att atg cta gat gta cag caa gag gag tat ctg ccc	672
Asn Gly Leu Glu Ile Met Leu Asp Val Gln Gln Glu Glu Tyr Leu Pro	
210 215 220	
atc tgg aag gac atg gaa gag acc ccg ttt gag gtg ggg atc cga gtg	720
Ile Trp Lys Asp Met Glu Glu Thr Pro Phe Glu Val Gly Ile Arg Val	
225 230 235 240	
cag att cac agc cag gat gag ccc cct gcc att gac cag ctg ggc ttc	768
Gln Ile His Ser Gln Asp Glu Pro Pro Ala Ile Asp Gln Leu Gly Phe	
245 250 255	
ggg gca gcc cca ggc cat cag act ttt gtg tcc tgt cag cag cag caa	816
Gly Ala Ala Pro Gly His Gln Thr Phe Val Ser Cys Gln Gln Gln Gln	
260 265 270	
ctg agt ttc ctg cca cca ccc tgg ggt gac tgc aat acc gca tct ttg	864
Leu Ser Phe Leu Pro Pro Pro Trp Gly Asp Cys Asn Thr Ala Ser Leu	
275 280 285	
gat ccc gac gac ttt gat cca gag ccc tct gat ccc ttg ggt tcc ccc	912
Asp Pro Asp Asp Phe Asp Pro Glu Pro Ser Asp Pro Leu Gly Ser Pro	
290 295 300	
aga ccc aga ccc agc cct cct tat agt tta ata ggt tgt cgc ctg gcc	960
Arg Pro Arg Pro Ser Pro Pro Tyr Ser Leu Ile Gly Cys Arg Leu Ala	
305 310 315 320	
tgt gag tct cgc tat gtg gct cgg aag tgt ggc tgt cga atg atg cat	1008
Cys Glu Ser Arg Tyr Val Ala Arg Lys Cys Gly Cys Arg Met Met His	
325 330 335	
atg cct gga aac tcc cca gtg tgc agc ccc cag cag tac aag gac tgc	1056
Met Pro Gly Asn Ser Pro Val Cys Ser Pro Gln Gln Tyr Lys Asp Cys	
340 345 350	

gcc agc cca gct ctg gac gct atg ctg cga aag gac acg tgt gtc tgc 1104
 Ala Ser Pro Ala Leu Asp Ala Met Leu Arg Lys Asp Thr Cys Val Cys
 355 360 365

 ccc aac ccg tgc gct act aca cgc tat gcc aag gag ctc tcc atg gtg 1152
 Pro Asn Pro Cys Ala Thr Thr Arg Tyr Ala Lys Glu Leu Ser Met Val
 370 375 380

 cgg att ccc agc cgc gcg tca gct cgc tac ctg gcc cgg aaa tac aac 1200
 Arg Ile Pro Ser Arg Ala Ser Ala Arg Tyr Leu Ala Arg Lys Tyr Asn
 385 390 395 400

 cgc agc gag tcc tac att acg gag aat gta ctg gtt ctg gat atc ttc 1248
 Arg Ser Glu Ser Tyr Ile Thr Glu Asn Val Leu Val Leu Asp Ile Phe
 405 410 415

 ttt gag gcc ctc aac tat gaa gcg gtg gaa caa aag gcg gcc tat gaa 1296
 Phe Glu Ala Leu Asn Tyr Glu Ala Val Glu Gln Lys Ala Ala Tyr Glu
 420 425 430

 gtg tcg gag ctg ctg gga gac att ggg gga cag atg gga ctg ttt att 1344
 Val Ser Glu Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile
 435 440 445

 gga gca agc ctg ctt acc atc ctt gag atc ctc gac tat ctc tgt gag 1392
 Gly Ala Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp Tyr Leu Cys Glu
 450 455 460

 gtt ttc caa gac aga gtc ctg ggg tat ttc tgg aac aga agg agc gct 1440
 Val Phe Gln Asp Arg Val Leu Gly Tyr Phe Trp Asn Arg Arg Ser Ala
 465 470 475 480

 caa aag cgc tct ggc aac act ctg ctc cag gaa gag ttg aat ggc cat 1488
 Gln Lys Arg Ser Gly Asn Thr Leu Leu Gln Glu Glu Leu Asn Gly His
 485 490 495

 cga aca cat gtt ccc cac ctc agc cta ggg ccc agg cct cct acc act 1536
 Arg Thr His Val Pro His Leu Ser Leu Gly Pro Arg Pro Pro Thr Thr
 500 505 510

 ccc tgt gct gtc acc aag aca ctc tct gcc tcc cac cgt acc tgt tac 1584
 Pro Cys Ala Val Thr Lys Thr Leu Ser Ala Ser His Arg Thr Cys Tyr
 515 520 525

 ctc gtc aca agg ctc tag 1602
 Leu Val Thr Arg Leu
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 <213> rat

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 Asp Ile Arg Val Phe Ala Ser Ser Cys Thr Met His Gly Leu Gly His
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Ile	Phe	Gly	Pro	Gly	Gly	Leu	Thr	Leu	Arg	Arg	Gly	Leu	Trp	Ala	Thr	35	40	45
Ala	Val	Leu	Leu	Ser	Leu	Ala	Ala	Phe	Leu	Tyr	Gln	Val	Ala	Glu	Arg	50	55	60
Val	Arg	Tyr	Tyr	Gly	Glu	Phe	His	His	Lys	Thr	Thr	Leu	Asp	Glu	Arg	65	70	75
Glu	Ser	His	Gln	Leu	Thr	Phe	Pro	Ala	Val	Thr	Leu	Cys	Asn	Ile	Asn	85	90	95
Pro	Leu	Arg	Arg	Ser	Arg	Leu	Thr	Pro	Asn	Asp	Leu	His	Trp	Ala	Gly	100	105	110
Thr	Ala	Leu	Leu	Gly	Leu	Asp	Pro	Ala	Glu	His	Ala	Ala	Tyr	Leu	Arg	115	120	125
Ala	Leu	Gly	Gln	Pro	Pro	Ala	Pro	Pro	Gly	Phe	Met	Pro	Ser	Pro	Thr	130	135	140
Phe	Asp	Met	Ala	Gln	Leu	Tyr	Ala	Arg	Ala	Gly	His	Ser	Leu	Glu	Asp	145	150	155
Met	Leu	Leu	Asp	Cys	Arg	Tyr	Arg	Gly	Gln	Pro	Cys	Gly	Pro	Glu	Asn	165	170	175
Phe	Thr	Val	Ile	Phe	Thr	Arg	Met	Gly	Gln	Cys	Tyr	Thr	Phe	Asn	Ser	180	185	190
Gly	Ala	His	Gly	Ala	Glu	Leu	Leu	Thr	Thr	Pro	Lys	Gly	Gly	Ala	Gly	195	200	205
Asn	Gly	Leu	Glu	Ile	Met	Leu	Asp	Val	Gln	Gln	Glu	Glu	Tyr	Leu	Pro	210	215	220
Ile	Trp	Lys	Asp	Met	Glu	Glu	Thr	Pro	Phe	Glu	Val	Gly	Ile	Arg	Val	225	230	235
Gln	Ile	His	Ser	Gln	Asp	Glu	Pro	Pro	Ala	Ile	Asp	Gln	Leu	Gly	Phe	245	250	255
Gly	Ala	Ala	Pro	Gly	His	Gln	Thr	Phe	Val	Ser	Cys	Gln	Gln	Gln	Gln	260	265	270
Leu	Ser	Phe	Leu	Pro	Pro	Pro	Trp	Gly	Asp	Cys	Asn	Thr	Ala	Ser	Leu	275	280	285
Asp	Pro	Asp	Asp	Phe	Asp	Pro	Glu	Pro	Ser	Asp	Pro	Leu	Gly	Ser	Pro	290	295	300
Arg	Pro	Arg	Pro	Ser	Pro	Pro	Tyr	Ser	Leu	Ile	Gly	Cys	Arg	Leu	Ala	305	310	315
Cys	Glu	Ser	Arg	Tyr	Val	Ala	Arg	Lys	Cys	Gly	Cys	Arg	Met	Met	His	325	330	335
Met	Pro	Gly	Asn	Ser	Pro	Val	Cys	Ser	Pro	Gln	Gln	Tyr	Lys	Asp	Cys	340	345	350

Ala Ser Pro Ala Leu Asp Ala Met Leu Arg Lys Asp Thr Cys Val Cys
355 360 365

Pro Asn Pro Cys Ala Thr Thr Arg Tyr Ala Lys Glu Leu Ser Met Val
370 375 380

Arg Ile Pro Ser Arg Ala Ser Ala Arg Tyr Leu Ala Arg Lys Tyr Asn
385 390 395 400

Arg Ser Glu Ser Tyr Ile Thr Glu Asn Val Leu Val Leu Asp Ile Phe
405 410 415

Phe Glu Ala Leu Asn Tyr Glu Ala Val Glu Gln Lys Ala Ala Tyr Glu
420 425 430

Val Ser Glu Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile
435 440 445

Gly Ala Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp Tyr Leu Cys Glu
450 455 460

Val Phe Gln Asp Arg Val Leu Gly Tyr Phe Trp Asn Arg Arg Ser Ala
465 470 475 480

Gln Lys Arg Ser Gly Asn Thr Leu Leu Gln Glu Glu Leu Asn Gly His
485 490 495

Arg Thr His Val Pro His Leu Ser Leu Gly Pro Arg Pro Pro Thr Thr
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Pro Cys Ala Val Thr Lys Thr Leu Ser Ala Ser His Arg Thr Cys Tyr
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Leu Val Thr Arg Leu
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<212> DNA
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<222> (16)..(1704)

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Met Ser Arg Ser Gly Gly Ala Arg Leu Pro Ala Thr
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gcg ctc agc ggc ccg gga cgc ttc cgt atg gcc cgc gag cag ccg gcg 99
Ala Leu Ser Gly Pro Gly Arg Phe Arg Met Ala Arg Glu Gln Pro Ala
15 20 25

ccc gtg gcg gtg gcg gca gct agg cag ccc gga gga gac cgg agc ggc 147
Pro Val Ala Val Ala Ala Arg Gln Pro Gly Gly Asp Arg Ser Gly
30 35 40

gat	ccg	gcg	ctg	cag	ggg	cca	ggg	gtc	gcc	cgc	agg	ggg	cgg	ccg	tcc	195
Asp	Pro	Ala	Leu	Gln	Gly	Pro	Gly	Val	Ala	Arg	Arg	Gly	Arg	Pro	Ser	
45					50					55					60	
ctg	agt	cgc	act	aaa	ttg	cac	ggg	ctg	cgg	cac	atg	tgc	gcg	ggg	cgc	243
Leu	Ser	Arg	Thr	Lys	Leu	His	Gly	Leu	Arg	His	Met	Cys	Ala	Gly	Arg	
				65					70					75		
acg	gcg	gcg	gga	ggc	tct	ttc	cag	cga	cgg	gcg	ctg	tgg	gtg	ctg	gcc	291
Thr	Ala	Ala	Gly	Gly	Ser	Phe	Gln	Arg	Arg	Ala	Leu	Trp	Val	Leu	Ala	
			80					85					90			
ttc	tgc	acg	tcc	ctc	ggc	ttg	ctg	ctg	tcc	tgg	tcc	tcg	aac	cgc	ctg	339
Phe	Cys	Thr	Ser	Leu	Gly	Leu	Leu	Leu	Ser	Trp	Ser	Ser	Asn	Arg	Leu	
		95					100					105				
ctc	tac	tgg	ctc	agc	ttc	ccg	tca	cac	aca	cga	gtg	cac	cgt	gag	tgg	387
Leu	Tyr	Trp	Leu	Ser	Phe	Pro	Ser	His	Thr	Arg	Val	His	Arg	Glu	Trp	
	110					115					120					
agc	cgc	cag	ctg	ccg	ttc	ccc	gcc	gtc	acc	gtg	tgc	aac	aac	aac	ccc	435
Ser	Arg	Gln	Leu	Pro	Phe	Pro	Ala	Val	Thr	Val	Cys	Asn	Asn	Asn	Pro	
125					130					135					140	
ctg	cgc	ttc	ccg	cgc	ctc	tcc	aag	ggg	gac	ctc	tac	tac	gcg	ggc	cac	483
Leu	Arg	Phe	Pro	Arg	Leu	Ser	Lys	Gly	Asp	Leu	Tyr	Tyr	Ala	Gly	His	
				145					150					155		
tgg	cta	ggg	ctg	ctg	ctt	ccc	aac	cgc	acc	gcg	cgc	ccg	ctg	gtc	agc	531
Trp	Leu	Gly	Leu	Leu	Leu	Pro	Asn	Arg	Thr	Ala	Arg	Pro	Leu	Val	Ser	
			160					165					170			
gag	ctg	ctg	cgg	ggc	gac	gag	ccg	cgc	cgc	cag	tgg	ttc	cgc	aaa	ctg	579
Glu	Leu	Leu	Arg	Gly	Asp	Glu	Pro	Arg	Arg	Gln	Trp	Phe	Arg	Lys	Leu	
		175					180					185				
gcc	gac	ttc	cgc	ctc	ttc	ctg	ccg	ccg	cgc	cac	ttc	gag	ggc	atc	agc	627
Ala	Asp	Phe	Arg	Leu	Phe	Leu	Pro	Pro	Arg	His	Phe	Glu	Gly	Ile	Ser	
	190					195					200					
gct	gcc	ttc	atg	gac	cgt	ttg	ggc	cac	cag	ctg	gag	gat	atg	ctg	ctc	675
Ala	Ala	Phe	Met	Asp	Arg	Leu	Gly	His	Gln	Leu	Glu	Asp	Met	Leu	Leu	
205					210					215				220		
tcc	tgc	aag	tac	cgg	ggc	gag	ctc	tgt	ggc	ccg	cac	aac	ttc	tcc	tca	723
Ser	Cys	Lys	Tyr	Arg	Gly	Glu	Leu	Cys	Gly	Pro	His	Asn	Phe	Ser	Ser	
				225					230					235		
gtg	ttt	aca	aaa	tac	ggg	aag	tgt	tac	atg	ttt	aac	tca	ggc	gag	gat	771
Val	Phe	Thr	Lys	Tyr	Gly	Lys	Cys	Tyr	Met	Phe	Asn	Ser	Gly	Glu	Asp	
			240					245					250			
ggc	aag	ccg	ctg	ctc	acc	acg	gtc	aag	ggg	ggg	acg	ggc	aac	ggg	ctg	819
Gly	Lys	Pro	Leu	Leu	Thr	Thr	Val	Lys	Gly	Gly	Thr	Gly	Asn	Gly	Leu	
		255					260					265				
gag	atc	atg	ctg	gac	att	cag	caa	gat	gag	tac	ctg	ccc	atc	tgg	gga	867
Glu	Ile	Met	Leu	Asp	Ile	Gln	Gln	Asp	Glu	Tyr	Leu	Pro	Ile	Trp	Gly	
	270					275					280					

gag aca gag gaa aca acg ttt gaa gca gga gtg aag gtt cag atc cac	915
Glu Thr Glu Glu Thr Thr Phe Glu Ala Gly Val Lys Val Gln Ile His	
285 290 295 300	
agt cag tct gag ccg cct ttc atc caa gag ctg ggc ttt ggg gtg gct	963
Ser Gln Ser Glu Pro Pro Phe Ile Gln Glu Leu Gly Phe Gly Val Ala	
305 310 315	
ccg ggg ttc cag acc ttc gtg gcc aca caa gag cag agg ctc aca tat	1011
Pro Gly Phe Gln Thr Phe Val Ala Thr Gln Glu Gln Arg Leu Thr Tyr	
320 325 330	
ctg ccc cca cca tgg ggg gag tgc cgg tcc tca gag atg gga ctc gac	1059
Leu Pro Pro Pro Trp Gly Glu Cys Arg Ser Ser Glu Met Gly Leu Asp	
335 340 345	
ttc ttt cct gtt tac agc atc aca gcc tgt cgg att gac tgt gag acc	1107
Phe Phe Pro Val Tyr Ser Ile Thr Ala Cys Arg Ile Asp Cys Glu Thr	
350 355 360	
cgc tac atc gtg gag aac tgt aac tgc cgc atg gtc cac atg cca ggg	1155
Arg Tyr Ile Val Glu Asn Cys Asn Cys Arg Met Val His Met Pro Gly	
365 370 375 380	
gac gcc cct ttc tgc acc cct gag cag cac aag gag tgt gca gag cct	1203
Asp Ala Pro Phe Cys Thr Pro Glu Gln His Lys Glu Cys Ala Glu Pro	
385 390 395	
gcc ctc ggt cta ctg gca gaa aag gac agc aat tac tgt ctc tgc agg	1251
Ala Leu Gly Leu Leu Ala Glu Lys Asp Ser Asn Tyr Cys Leu Cys Arg	
400 405 410	
aca ccc tgc aac ctg aca cgc tac aac aaa gag ctc tcc atg gtg aag	1299
Thr Pro Cys Asn Leu Thr Arg Tyr Asn Lys Glu Leu Ser Met Val Lys	
415 420 425	
atc ccc agc aag acg tca gcc aag tac tta gag aag aaa ttt aac aaa	1347
Ile Pro Ser Lys Thr Ser Ala Lys Tyr Leu Glu Lys Lys Phe Asn Lys	
430 435 440	
tcg gaa aaa tat atc tca gag aac att ctt gtt ctg gac ata ttt ttt	1395
Ser Glu Lys Tyr Ile Ser Glu Asn Ile Leu Val Leu Asp Ile Phe Phe	
445 450 455 460	
gag gcg ctc aat tac gaa aca att gaa cag aag aag gcg tat gaa gtt	1443
Glu Ala Leu Asn Tyr Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Val	
465 470 475	
gct gcc tta ctt ggt gac atc ggt ggt cag atg gga ctg ttc att ggt	1491
Ala Ala Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly	
480 485 490	
gct agt ctc ctc aca ata cta gag ctc ttt gat tat att tat gag ctg	1539
Ala Ser Leu Leu Thr Ile Leu Glu Leu Phe Asp Tyr Ile Tyr Glu Leu	
495 500 505	
atc aaa gag aag cta tta gac ctg ctt ggc aaa gaa gaa gag gaa ggg	1587
Ile Lys Glu Lys Leu Leu Asp Leu Leu Gly Lys Glu Glu Glu Glu Gly	
510 515 520	

agc cac gat gag aac atg agc acc tgt gac aca atg cca aac cac tct 1635
 Ser His Asp Glu Asn Met Ser Thr Cys Asp Thr Met Pro Asn His Ser
 525 530 535 540

gaa acc atc agc cac act gtg aac gtg ccc ctg cag aca gct ttg ggc 1683
 Glu Thr Ile Ser His Thr Val Asn Val Pro Leu Gln Thr Ala Leu Gly
 545 550 555

acc ctg gag gag att gcc tgc tgacacctct caggcaacgc agcacctcca 1734
 Thr Leu Glu Glu Ile Ala Cys
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aacagacctt aaaggcccaa gacctaggac aggagacagc aagcgcaggt gggatcgccc 1794

ctgacgactg aaagaagcag agccccccat atgcacacat tgcgaacttc tgccaaacct 1854

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atgagtcgca ctccggaact gtccaagaac taac 1948

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 <211> 563
 <212> PRT
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<400> 12

Met Ser Arg Ser Gly Gly Ala Arg Leu Pro Ala Thr Ala Leu Ser Gly
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Pro Gly Arg Phe Arg Met Ala Arg Glu Gln Pro Ala Pro Val Ala Val
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 35 40 45

Gln Gly Pro Gly Val Ala Arg Arg Gly Arg Pro Ser Leu Ser Arg Thr
 50 55 60

Lys Leu His Gly Leu Arg His Met Cys Ala Gly Arg Thr Ala Ala Gly
 65 70 75 80

Gly Ser Phe Gln Arg Arg Ala Leu Trp Val Leu Ala Phe Cys Thr Ser
 85 90 95

Leu Gly Leu Leu Leu Ser Trp Ser Ser Asn Arg Leu Leu Tyr Trp Leu
 100 105 110

Ser Phe Pro Ser His Thr Arg Val His Arg Glu Trp Ser Arg Gln Leu
 115 120 125

Pro Phe Pro Ala Val Thr Val Cys Asn Asn Asn Pro Leu Arg Phe Pro
 130 135 140

Arg Leu Ser Lys Gly Asp Leu Tyr Tyr Ala Gly His Trp Leu Gly Leu
 145 150 155 160

Leu Leu Pro Asn Arg Thr Ala Arg Pro Leu Val Ser Glu Leu Leu Arg
 165 170 175

Gly Asp Glu Pro Arg Arg Gln Trp Phe Arg Lys Leu Ala Asp Phe Arg
 180 185 190
 Leu Phe Leu Pro Pro Arg His Phe Glu Gly Ile Ser Ala Ala Phe Met
 195 200 205
 Asp Arg Leu Gly His Gln Leu Glu Asp Met Leu Leu Ser Cys Lys Tyr
 210 215 220
 Arg Gly Glu Leu Cys Gly Pro His Asn Phe Ser Ser Val Phe Thr Lys
 225 230 235 240
 Tyr Gly Lys Cys Tyr Met Phe Asn Ser Gly Glu Asp Gly Lys Pro Leu
 245 250 255
 Leu Thr Thr Val Lys Gly Gly Thr Gly Asn Gly Leu Glu Ile Met Leu
 260 265 270
 Asp Ile Gln Gln Asp Glu Tyr Leu Pro Ile Trp Gly Glu Thr Glu Glu
 275 280 285
 Thr Thr Phe Glu Ala Gly Val Lys Val Gln Ile His Ser Gln Ser Glu
 290 295 300
 Pro Pro Phe Ile Gln Glu Leu Gly Phe Gly Val Ala Pro Gly Phe Gln
 305 310 315 320
 Thr Phe Val Ala Thr Gln Glu Gln Arg Leu Thr Tyr Leu Pro Pro Pro
 325 330 335
 Trp Gly Glu Cys Arg Ser Ser Glu Met Gly Leu Asp Phe Phe Pro Val
 340 345 350
 Tyr Ser Ile Thr Ala Cys Arg Ile Asp Cys Glu Thr Arg Tyr Ile Val
 355 360 365
 Glu Asn Cys Asn Cys Arg Met Val His Met Pro Gly Asp Ala Pro Phe
 370 375 380
 Cys Thr Pro Glu Gln His Lys Glu Cys Ala Glu Pro Ala Leu Gly Leu
 385 390 395 400
 Leu Ala Glu Lys Asp Ser Asn Tyr Cys Leu Cys Arg Thr Pro Cys Asn
 405 410 415
 Leu Thr Arg Tyr Asn Lys Glu Leu Ser Met Val Lys Ile Pro Ser Lys
 420 425 430
 Thr Ser Ala Lys Tyr Leu Glu Lys Lys Phe Asn Lys Ser Glu Lys Tyr
 435 440 445
 Ile Ser Glu Asn Ile Leu Val Leu Asp Ile Phe Phe Glu Ala Leu Asn
 450 455 460
 Tyr Glu Thr Ile Glu Gln Lys Lys Ala Tyr Glu Val Ala Ala Leu Leu
 465 470 475 480
 Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala Ser Leu Leu
 485 490 495

Thr Ile Leu Glu Leu Phe Asp Tyr Ile Tyr Glu Leu Ile Lys Glu Lys
500 505 510

Leu Leu Asp Leu Leu Gly Lys Glu Glu Glu Gly Ser His Asp Glu
515 520 525

Asn Met Ser Thr Cys Asp Thr Met Pro Asn His Ser Glu Thr Ile Ser
530 535 540

His Thr Val Asn Val Pro Leu Gln Thr Ala Leu Gly Thr Leu Glu Glu
545 550 555 560

Ile Ala Cys

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<212> PRT
<213> Helix aspersa

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His Gln His Ala Met Met Arg Asn Arg Tyr His Pro His His Cys Asn
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Tyr Ser Asp Asn Arg Ser Ala Ile Asp Ile Ile Ala Glu Leu Gly Ser
35 40 45

Glu Ser Asn Ala His Gly Leu Ala Lys Ile Val Thr Ser Arg Asp Thr
50 55 60

Lys Arg Lys Val Ile Trp Ala Leu Leu Val Ile Ala Gly Phe Thr Ala
65 70 75 80

Ala Thr Leu Gln Leu Ser Leu Leu Val Arg Lys Tyr Leu Gln Phe Gln
85 90 95

Val Val Glu Leu Ser Glu Ile Lys Asp Ser Met Pro Val Gln Tyr Pro
100 105 110

Ser Val Ser Ile Cys Asn Ile Glu Pro Ile Ser Leu Arg Thr Ile Arg
115 120 125

Arg Met Tyr Phe Asn Asn Glu Ser Gln Asn Leu Ile Thr Trp Leu Arg
130 135 140

Phe Ile Gln Lys Phe Arg Phe Glu Gln Asp Ser Phe Met Asn Ser Ile
145 150 155 160

Arg Ala Phe Tyr Glu Asn Leu Gly Gln Asp Ala Lys Lys Leu Ser His
165 170 175

Asn Leu Glu Asp Met Leu Met His Cys Arg Phe Asn Arg Glu Leu Cys
180 185 190

His Val Ser Asn Phe Ser Thr Phe Phe Asp Gly Asn Tyr Phe Asn Cys
195 200 205

Phe 210	Thr	Phe	Asn	Ser	Gly	Gln	Arg	Leu	Gln	Met	His 220	Ala	Thr	Gly	Pro
Glu 225	Asn	Gly	Leu	Ser	Leu 230	Ile	Phe	Ser	Val	Glu 235	Lys	Asp	Asp	Pro	Leu 240
Pro	Gly	Thr	Tyr	Gly 245	Val	Tyr	Asn	Phe	Asp 250	Asn	Asn	Ile	Leu	His 255	Ser
Ala	Gly	Val	Arg 260	Val	Val	Val	His	Ala 265	Pro	Gly	Ser	Met	Pro 270	Ser	Pro
Val	Asp	His 275	Gly	Ile	Asp	Ile	Pro 280	Pro	Gly	Tyr	Ser	Ser 285	Ser	Val	Gly
Leu	Lys 290	Ala	Ile	Leu	His	Thr 295	Arg	Leu	Pro	Tyr	Pro 300	Tyr	Gly	Asn	Cys
Thr 305	Asn	Asp	Met	Leu	Asn 310	Gly	Ile	Lys	Gln	Tyr 315	Lys	Tyr	Thr	Phe	Phe 320
Ala	Cys	Leu	Gln	Leu 325	Cys	Lys	Gln	Arg	Leu 330	Ile	Ile	Gln	Arg	Cys 335	Gly
Cys	Lys	Ser	Ser 340	Ala	Leu	Pro	Glu 345	Val	Pro	Ser	Tyr	Asn	Ala 350	Thr	Phe
Cys	Gly	Val 355	Ile	Lys	Asp	Trp	Gln 360	Glu	Ile	Asn	Arg	Asn 365	His	Ser	Asn
Glu 370	Asp	His	Asn	Gln	Ser	Glu 375	Glu	Asp	Arg	Ala	Phe 380	Ile	Pro	Thr	Pro
Tyr 385	Leu	Ala	Cys	Glu	Glu 390	Arg	Glu	Gln	Lys	Asn 395	Leu	Asn	Asn	Asp	Arg 400
Thr	Tyr	Glu	Leu	Ser 405	Cys	Gly	Cys	Phe	Gln 410	Pro	Cys	Ser	Glu	Thr 415	Ser
Tyr	Leu	Lys	Ser 420	Val	Ser	Leu	Ser	Tyr 425	Trp	Pro	Leu	Glu	Phe 430	Tyr	Gln
Leu	Ser	Ala 435	Val	Glu	Arg	Phe	Phe 440	Lys	Gln	Glu	Arg	Gln 445	Ala	Gly	Gln
Asn 450	His	Phe	Met	Lys	Thr	Ala 455	Tyr	Glu	Tyr	Leu	Glu 460	Lys	Leu	Ala	His
Pro 465	Ser	Gln	Lys	His	Leu 470	Ala	Arg	Asn	Asp	Ser 475	His	Met	Asp	Asp	Ile 480
Leu	Ser	Lys	Ser	Tyr 485	Ser	Leu	Ser	Glu	Lys 490	Glu	Met	Ala	Lys	Glu 495	Ala
Ser	Asp	Leu	Ile 500	Arg	Gln	Asn	Met	Leu 505	Arg	Leu	Asn	Ile	Tyr 510	Leu	Glu
Asp	Leu	Ser 515	Val	Val	Glu	Tyr	Arg 520	Gln	Leu	Pro	Ala 525	Tyr	Gly	Leu	Ala

Asp Leu Phe Ala Asp Ile Gly Gly Thr Leu Gly Leu Trp Met Gly Ile
 530 535 540
 Ser Val Leu Thr Ile Met Glu Leu Ile Glu Leu Val Ile Arg Leu Thr
 545 550 555 560
 Gly Leu Val Phe Asn Ser Glu Lys Gly Leu Pro Arg Gly Pro Thr Thr
 565 570 575
 Val Asn Asn Asn Asn Gly Ser Asn Asn His Ser Gln Ser Thr Ser Gln
 580 585 590
 His Gln Leu Tyr Asn Gly Tyr Met Asp His Asp Ser His Tyr Ser Asp
 595 600 605
 Ser Ala Gly Ala Ser Val Phe Asp Phe Arg Arg Gly Val Glu Ser Pro
 610 615 620
 Val
 625
 <210> 14
 <211> 564
 <212> PRT
 <213> C. elegans
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 Ser Glu Tyr Met Ser Gln Val Tyr Gly Asp Pro Leu Ala Tyr Leu Gln
 20 25 30
 Glu Asn Thr Lys Phe Val Thr Glu Arg Glu Tyr Tyr Glu Asp Phe Gly
 35 40 45
 Tyr Gly Glu Cys Phe Asn Ser Ser Glu Ser Glu Val Gln Cys Glu Leu
 50 55 60
 Ile Thr Gly Glu Phe Asp Pro Lys Leu Leu Pro Tyr Asp Lys Arg Leu
 65 70 75 80
 Ala Trp His Phe Lys Glu Phe Cys Tyr Lys Thr Ser Ala His Gly Ile
 85 90 95
 Pro Met Ile Gly Glu Ala Pro Asn Val Tyr Tyr Arg Ala Val Trp Val
 100 105 110
 Met Leu Phe Leu Gly Cys Met Ile Met Leu Tyr Leu Asn Ala Gln Ser
 115 120 125
 Val Leu Asp Lys Tyr Asn Arg Asn Glu Lys Ile Val Asp Ile Gln Leu
 130 135 140

Phe	Lys	Phe	Asp	Thr	Ala	Pro	Phe	Pro	Ala	Ile	Thr	Leu	Cys	Asn	Leu	145	150	155	160
Asn	Pro	Tyr	Lys	Ala	Ser	Leu	Ala	Thr	Ser	Val	Asp	Leu	Val	Lys	Arg	165	170	175	
Thr	Leu	Ser	Xaa	Glu	Ile	Trp	Thr	Tyr	Leu	Gln	Gly	Gly	Thr	Pro	Thr	180	185	190	
Glu	Asp	Pro	Asn	Phe	Leu	Glu	Ala	Met	Gly	Phe	Gln	Gly	Met	Thr	Asp	195	200	205	
Glu	Val	Ala	Ile	Val	Thr	Lys	Ala	Lys	Glu	Asn	Ile	Met	Phe	Ala	Met	210	215	220	
Ala	Thr	Leu	Ser	Met	Gln	Asp	Arg	Glu	Arg	Leu	Ser	Thr	Thr	Lys	Arg	225	230	235	240
Glu	Leu	Val	His	Lys	Cys	Ser	Phe	Asn	Gly	Lys	Ala	Cys	Asp	Ile	Glu	245	250	255	
Ala	Asp	Phe	Leu	Thr	His	Ile	Asp	Pro	Val	Phe	Gly	Ser	Cys	Phe	Thr	260	265	270	
Phe	Asn	His	Asn	Arg	Thr	Val	Asn	Leu	Thr	Ser	Ile	Arg	Ala	Gly	Pro	275	280	285	
Met	Tyr	Gly	Leu	Arg	Met	Leu	Val	Tyr	Val	Asn	Ala	Ser	Asp	Tyr	Met	290	295	300	
Pro	Thr	Thr	Glu	Ala	Thr	Gly	Val	Arg	Leu	Thr	Ile	His	Asp	Lys	Glu	305	310	315	320
Asp	Phe	Pro	Phe	Pro	Asp	Thr	Phe	Gly	Tyr	Ser	Ala	Pro	Thr	Gly	Tyr	325	330	335	
Val	Ser	Ser	Phe	Gly	Leu	Arg	Leu	Arg	Lys	Met	Ser	Arg	Leu	Pro	Ala	340	345	350	
Pro	Tyr	Gly	Asp	Cys	Val	Pro	Asp	Gly	Lys	Thr	Ser	Asp	Tyr	Ile	Tyr	355	360	365	
Ser	Asn	Tyr	Glu	Tyr	Ser	Val	Glu	Gly	Cys	Tyr	Arg	Ser	Cys	Phe	Gln	370	375	380	
Gln	Leu	Val	Leu	Lys	Glu	Cys	Arg	Cys	Gly	Asp	Pro	Arg	Phe	Pro	Val	385	390	395	400
Pro	Glu	Gly	Ala	Arg	His	Cys	Asp	Ala	Ala	Asp	Pro	Val	Ala	Arg	Arg	405	410	415	
Cys	Leu	Asp	Ala	Arg	Met	Asn	Asp	Leu	Gly	Gly	Leu	His	Gly	Ser	Phe	420	425	430	
Arg	Cys	Arg	Cys	Gln	Gln	Pro	Cys	Gly	Gln	Ser	Ile	Tyr	Ser	Val	Thr	435	440	445	
Tyr	Ser	Pro	Ala	Lys	Trp	Pro	Ser	Leu	Ser	Leu	Gln	Ile	Gln	Leu	Gly	450	455	460	

Ser Cys Asn Gly Thr Ala Val Glu Cys Asn Lys His Tyr Lys Glu Asn
 465 470 475 480
 Gly Ala Met Val Glu Val Phe Tyr Glu Gln Leu Asn Phe Glu Met Leu
 485 490 495
 Thr Glu Ser Glu Ala Tyr Gly Phe Val Asn Leu Leu Ala Asp Phe Gly
 500 505 510
 Gly Gln Leu Gly Leu Trp Cys Gly Ile Ser Phe Leu Thr Cys Cys Glu
 515 520 525
 Phe Val Phe Leu Phe Leu Glu Thr Ala Tyr Met Ser Ala Glu His Asn
 530 535 540
 Tyr Ser Leu Tyr Lys Lys Lys Lys Ala Glu Lys Ala Lys Lys Val Ala
 545 550 555 560
 Ser Gly Ser Phe

<210> 15
 <211> 24
 <212> DNA
 <213> degenerate primer

<220>
 <221> modified_base
 <222> (various_positions)
 <223> "n" at positions 6, 9, 12, 15 & 16 represents
 "inosine", while "n" at position 18 represents A,
 T, C, G or unknown

<400> 15
 ttyccngcncr tnacnntntg yaay

24

<210> 16
 <211> 26
 <212> DNA
 <213> degenerate primer

<220>
 <221> modified_base
 <222> (various_positions)
 <223> "n" at positions 3, 6, 9, 11 & 12 represents
 "inosine", while "n" at positions 15 & 18 represents A,
 T, C, G or unknown

<400> 16
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26

<210> 17
 <211> 20
 <212> DNA
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<400> 17
 attgctcttc ccatctctat

20

~~<210> 18
<211> 20
<212> DNA
<213> primer~~

<400> 18
ttcaaggccc atacctaagt

20

Full
CID
cont